

## **REMARKS**

Claims 1-33 have been canceled. Claims 34 and 35 are newly added. Reconsideration and withdrawal of the rejections set forth in the Office Action dated August 23, 2005 are respectfully requested.

### **I. Amendments**

Claims 34 and 35 are newly added. Support for the newly added claims may be found in the claims as originally filed, as well as on p. 16, lines 8-16 of the Specification.

### **II. Restriction/Election**

Applicants have acknowledged the Examiner's arguments with respect to the restriction and election imposed in the instant application. Applicants have elected to pursue Group I, drawn to nucleic acid(s), vector, expression system and method of use.

### **III. Filing Date**

Applicants note that the filing date on the Office Action mailed August 23, 2005 is incorrect. The filing date of the instant application is January 24, 2001, not May 25, 2001. On May 24, 2001, Applicants' representative filed a second preliminary amendment which submitted that the application was complete as of the accorded filing date of January 24, 2001. As such, Applicants request clarification regarding the filing date as noted on the Office Action mailed August 23, 2005.

### **IV. Rejection under 35 U.S.C. §112, first paragraph**

Claim 25 is rejected under 35 U.S.C. §112, first paragraph, as allegedly failing to comply with the written description requirement. Without acquiescing to this rejection and the reasons given therefor, claim 25 has been canceled with entry of this Amendment and the rejection is thereby moot. Therefore, Applicants respectfully request withdrawal of this rejection.

V. Rejections under 35 U.S.C. §102

Claim 25 is rejected under 35 U.S.C. §102(b) as allegedly being anticipated by Genseq database Accession No: AAQ27436 and GenEMBL D10333. This rejection is respectfully traversed for the following reasons. The Alignment sent by the Examiner has only compared the terminal portion of SEQ ID NO:15 beginning with residue 296 to Genseq database Accession No: AAQ27436. Applicants have created an alignment (see Exhibit A) between SEQ ID NO:15 and Genseq database Accession No: AAQ27436 ("gi" number 391711). The entire length of the protein is 549 residues. 230 matches divided by 549 residues is 41.89%. As such, Applicants' sequence shares less than 50% identity with the cited art when measured across the length of the entire sequence.

With respect to SEQ ID NO:16, the Examiner has sent an alignment that does not contain any numerical values or a percent identity summary. To verify the percent identity quoted by the Examiner, which is 92.74%, Applicants would like to create a protein-protein alignment using the entire amino acid sequence of SEQ ID NO:16, which contains 549 amino acid residues, and a program such as ClustalW, not a protein-nucleic acid crossed alignment. GenEMBL (Genbank) Accession No. D10333 is "gi" number 391711. Such an alignment is not 92.74% identical across the entire length of the protein. (see Exhibit B).

Further, without acquiescing to this rejection and the reasons given therefor, claim 25 has been canceled with entry of this Amendment. Therefore, Applicants respectfully request withdrawal of this rejection.

VI. Conclusion

In view of the foregoing, Applicants submit that the claims pending in the application comply with the requirements of 35 U.S.C. §112 and patentably define over the prior art. A Notice of Allowance is therefore respectfully requested.

If in the opinion of the Examiner, a telephone conference would expedite the prosecution of the subject application, the Examiner is encouraged to call the undersigned at (650) 838-4341.

Respectfully submitted,  
Perkins Coie LLP

Date: November 23, 2005

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# ClustalW Multiple Sequence Alignment Results

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Page 1.1

	1	15 16	30 31	45 46	60 61
1 gi 391711	-----	-----	-----	-----	---
2 SEQIDNO15	AVAPAHDTTPVPD	SRGAILRRQYNL	PLTSSVATGTNL	AAPLSPLLPLQD	THI

Page 2.1

	91	105 106	120 121	135 136	150 151
1 gi 391711	-----	-----	-----	-----	---
2 SEQIDNO15	VGGYAIISIFWPQ	TTPTSVDMNSIT	VRILVQPGIASL	PSERLHYRNQGW	ETS

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	181	195 196	210 211	225 226	240 241
1 gi 391711	-----	-----	-----	-----	---
2 SEQIDNO15	PYTGALGLLDFA	EFRLNTPGNTN	RYSSTARHRLRR	GTAELTTTAATR	FLY

Page 4.1

	271	285 286	300 301	315 316	330 331
1 gi 391711	-----	-----	-----	-----	---
2 SEQIDNO15	GLPTELISSAGG	YSRPVVSANGE	LYTSVENAQDQK	IPHDIDLGESRV	VIQ

Page 5.1

	361	375 376	390 391	405 406	420 421
1 gi 391711	WLSLTAAEYDQ	SSTGPVYVSDS	NVATGAQAVAR	TKVTLDGRPLST	IQQ
2 SEQIDNO15	WLSLTAAEYDQ	SSTGPVYVSDS	NVATGAQAVAR	TKVTLDGRPLST	IQQ

Page 6.1

	451	465 466	480 481	495 496	510 511
1 gi 391711	NTTASDQLLVEN	HRVAISTYTTSL	PVSISAVAVLAP	LALLEDTLDPAC	AH
2 SEQIDNO15	NTTASDQLLVEN	HRVAISTYTTSL	PVSISAVAVLAP	LALLEDTLDPAR	AH

Page 7.1

	541	555 556	570 571	585 586	600 601
1 gi 391711	MKV-----	248			
2 SEQIDNO15	MKVGKTREL	549			

### Alignment Data (Fasta format)

```
>gi|391711|
-----
-----
-----
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```

```
-----EPTVK
LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRP
FSVLRANDVLWLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVA
RSLDWTKVTL DGRPLSTIQQYSKTF FVLPLRGKLSFWEAGTTKAGYPYNY
NTTASDQLLVENAAGHRVAISTYTTSLGAGPVSISAVAVLAPHSALALLE
DTLDYPACAHTFDDDFCPECRPLGLQGCAFQSTVAELQRLKMKV-----
>SEQIDNO15|
AVAPAHDTPPVPDVS RGA ILRRQYNLSTSP L TSSVATGTNLVLYAAPLS
PLLPLQDGTNTHIMATEASNYAQYRVARATIRYRPLVPNAVGGYAI S I S F
WPQTTTTTPTSVD MNSITSTDVRI LVQPGIASELVIPSERLHYRNQGWRSV
ETSGVAEEEEATSGLVMLCIHGSLVNSYTNTPYT GALGLLDFALELEFRNL
TPGNTNTRVSRYSSSTARHRLRRGADGTAE LTTTAATRFMKDLYFTSTNGV
GEIGRGIALTLFNLADTL L GGLPTEL I S SAGGQLFYSRPVVSANGEPTVK
LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRP
FSVLRANDVLWLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVA
RSLDWTKVTL DGRPLSTIQQYSKTF FVLPLRGKLSFWEAGTTKAGYPYNY
NTTASDQLLVENAAGHRVAISTYTTSLGAGPVSISAVAVLAPHSALALLE
DTLDYPARAHTFDDDFCPECRPLGLQGCAFQSTVAELQRLKMKVGKTREL
```

[Try the BCM JAVA Alignment Viewer and Editor](#)

To prepare a publishable output of this alignment, try the [BOXSHADE](#) server.  
Copy the alignment output (highlighted in green) and choose 'other' for Input sequence format.

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**Kim C. Worley and Michael P. McLeod**, Human Genome Sequencing Center, Baylor College of Medicine  
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# ClustalW Multiple Sequence Alignment Results

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Page 1.1

```
      1           15 16           30 31           45 46           60 61
1 gi391711  -----
2 SEQIDNO16 AVAPAHDTSPVPDVS SRGAILRRQYNLSTS PLTSSVASGTNLVLY AAPLNPPPLPLQDGTN THIM
```

☐

Page 2.1

```
      91           105 106           120 121           135 136           150 151
1 gi391711  -----
2 SEQIDNO16 VGGYAISISFWPQTT TTPTSVDMSITSTD VRILVQPGIASELVI PSERLHYRNQGWRSV ETSG
```

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Page 3.1

```
     181           195 196           210 211           225 226           240 241
1 gi391711  -----
2 SEQIDNO16 PYTGALGLLDFALEL EFRNLTTCTNTRVS RYSSTARHRLRRGAD GTAELTTTAATRFMK DLHF
```

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Page 4.1

```
     271           285 286           300 301           315 316           330 331
1 gi391711  -----EPTVK LYTSVENAQQDKGIA IPHDIDLGESRVVIQ DYDN
2 SEQIDNO16 GLPTELISSAGGQLF YSRPVVSANGEPTVK LYTSVENAQQDKGVA IPHDIDLGDSRVVIQ DYDN
```

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Page 5.1

```
     361           375 376           390 391           405 406           420 421
1 gi391711  WLSLTAAEYDQSTYG SSTGPVYVSDSVTLV NVATGAQAVARSLDW TKVTLDGRPLSTIQQ YSKT
2 SEQIDNO16 WLSLTAAEYDQSTYG SSTGPVYISDSVTLV NVATGAQAVARSLDW SKVTLDGRPLPTVEQ YSKT
```

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Page 6.1

```
     451           465 466           480 481           495 496           510 511
1 gi391711  NTTASDQLLVENAAG HRVAISTYTTSLGAG PVSISAVAVLAPHA LALLEDTLDPACAH TFDD
2 SEQIDNO16 NTTASDQILIENAAG HRVAISTYTTTLGAG PVAISAAVLAPRSA LALLEDTFDYPGRAH TFDD
```

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Page 7.1

```
     541           555 556           570 571           585 586           600 601
1 gi391711  MKV----- 248
2 SEQIDNO16 VKVGKTREL 549
```

### Alignment Data (Fasta format)

>gi391711

```
-----
-----
-----
-----
```

```
-----EPTVK
LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTSPAPSRP
FSVLRANDVLWLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVA
RSLDWTQVTLTLDGRPLSTIQYQSKTFFVLPLRGKLSFWEAGTTKAGYPYNY
NTTASDQLLVENAAGHRVAISTYTTSLGAGPVSISAVAVLAPHSALALLE
DTLDYPACAHTFDDFCPECRPLGLQGCAFQSTVAELQRLKMKV-----
>SEQIDNO16
AVAPAHDTSPVPDVSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLN
PPLPLQDGTNTHIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISF
WPQTTTTPTSDMNSITSTDVRILVQPGIASLVIPSERLHYRNQGWRSV
ETSGVAEEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRNL
TTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMKDLHFTGLNGV
GEVGRGIALTLNLADTLGLLPTELISSAGGQLFYSRPVVSANGEPTVK
LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTSPAPSRP
FSVLRANDVLWLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVA
RSLDWSKVTLTLDGRPLPTVEQYQSKTFFVLPLRGKLSFWEAGTTKAGYPYNY
NTTASDQILIENTAAGHRVAISTYTTTLGAGPVAISAAVLAPRSALALLE
DTFDYPGRAHTFDDFCPECRALGLQGCAFQSTVAELQRLKVKGKTREL
```

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